CLEAN VERSION OF CLAIM AMENDMENTS

C2

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) a first nucleotide sequence which is a polymorphic variant of a reference sequence for the β_2-Adrenergic receptor (β_2AR) gene, wherein the polymorphic variant is a β_2AR isogene that encodes a β_2AR polypeptide capable of being activated by a β-agonist, wherein the first nucleotide sequence is selected from the group consisting of SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, and SEQ ID NO:28; and

(b) a second nucleotide sequence which is complementary to the first nucleotide sequence.

C3

29. A genome anthology for the β_2-Adrenergic Receptor gene (β_2-AR) gene which comprises a set of β_2-AR isogenes defined by haplotypes 1-12 shown in Table 5, wherein each of the β_2AR isogenes encodes a β_2-AR polypeptide capable of being activated by a β-agonist.

C4

33. The genome anthology of claim 29, wherein each isogene in the set is stored in a separate container.

ID NO:25, SEQ ID NO:26, SEQ ID NO:27, and SEQ ID NO:28;

and

(b) a second nucleotide sequence which is complementary to the first nucleotide sequence.

29. (amended) A genome anthology for the β_2-Adrenergic Receptor gene (β_2-AR) gene which comprises a set of β_2-AR isogenes defined by haplotypes 1-12 shown in Table 5, wherein each of the β_2AR isogenes encodes a β_2-AR polypeptide capable of being activated by a β-agonist.

Please add new dependent claim 33 as shown:

33. (new) The genome anthology of claim 29, wherein each isogene in the set is stored in a separate container.

A clean version of the claim amendments is attached hereto.

REMARKS

Replacement Sequence Listing

Applicants have determined that the previously submitted SEQ ID NOS:19-30, which are for the β_2-AR isogenes recited in the claims, unintentionally contained a larger region of the β_2-AR gene than the region described by the specification as being sequenced. *See* p. 33, lines 3-5. In addition, it was discovered that some of the isogenes have been previously reported and are not part of the claimed invention as described in the specification at p. 11, lines 22-25 and in the attached IDS. Thus, replacement SEQ ID NOS:19-28 correspond to novel isogenes comprising the minimum length of the region of the β_2-AR gene that Applicants sequenced and examined for polymorphisms and haplotypes, e.g., starting with polymorphic site 1 at nucleotide 565 in Figure 1 and ending with polymorphic site 13 at nucleotide 2110 in Figure 1. Support for this amendment to the Sequence Listing is found at p. 33, lines 3-5 and lines 23-27; p. 34, Table 3 and in Example 2 from line 5 on p. 34 to line 21 on p. 36. All the other SEQ ID NOS in the replacement sequence listing are identical to those originally filed. It is believed that no new matter is entered by this replacement sequence listing and its entry is respectfully requested.